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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: The Wistar Institute
Bayer Corporation

(ii) TITLE OF INVENTION: Peptides and Peptidomimetics with Structural Similarity to Human p53 That Activate p53 Function

(iii) NUMBER OF SEQUENCES: 35

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Banner & Allegretti, Ltd.
(B) STREET: 1001 G Street, N.W.
(C) CITY: Washington, D.C.
(D) STATE: District of Columbia
(E) COUNTRY: U.S.
(F) ZIP: 20001

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA: PCT
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA: USA
(A) APPLICATION NUMBER: 08/392,542
(B) FILING DATE: 02-16-95

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Hoscheit, Dale H.
(B) REGISTRATION NUMBER: 19,090
(C) REFERENCE/DOCKET NUMBER: 0486.53880

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202 508-9100
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCTAGAGCC ACCGTCCAGG GAGCAGGTAG CTGCTGGGCT CCGGGGACAC TTTGCGTTCG 60

GGCTGGGAGC GTGCTTTCCA CGACGGTGAC ACGCTTCCCT GGATTGGCAG CCAGACTGCC 120

TTCCGGGTCA CTGCCATGGA GGAGCCGCAG TCAGATCCTA GCGTCGAGCC CCCTCTGAGT 180

CAGGAAACAT TTTCAGACCT ATGGAAACTA CTTCCTGAAA ACAACGTTCT GTCCCCCTTG 240

CCGTCCCAAG CAATGGATGA TTTGATGCTG TCCCCGGACG ATATTGAACA ATGGTTCACT 300

GAAGACCCAG GTCCAGATGA AGCTCCCAGA ATGCCAGAGG CTGCTCCCCC CGTGGCCCCT 360

GCACCAGCAG CTCCTACACC GGCGGCCCCT GCACCAGCCC CCTCCTGGCC CCTGTCATCT 420

TCTGTCCCTT CCCAGAAAAC CTACCAGGGC AGCTACGGTT TCCGTCTGGG CTTCTTGCAT 480

TCTGGGACAG CCAAGTCTGT GACTTGCACG TACTCCCCTG CCCTCAACAA GATGTTTTGC 540

CAACTGGCCA AGACCTGCCC TGTGCAGCTG TGGGTTGATT CCACACCCCC GCCCGGCACC 600

CGCGTCCGCG CCATGGCCAT CTACAAGCAG TCACAGCACA TGACGGAGGT TGTGAGGCGC 660

TGCCCCCACC ATGAGCGCTG CTCAGATAGC GATGGTCTGG CCCCTCCTCA GCATCTTATC 720

CGAGTGGAAG GAAATTTGCG TGTGGAGTAT TTGGATGACA GAAACACTTT TCGACATAGT 780

GTGGTGGTGC CCTATGAGCC GCCTGAGGTT GGCTCTGACT GTACCACCAT CCACTACAAC 840

TACATGTGTA ACAGTTCCTG CATGGGCGGC ATGAACCGGA GGCCCATCCT CACCATCATC 900

ACACTGGAAG ACTCCAGTGG TAATCTACTG GGACGGAACA GCTTTGAGGT GCGTGTTTGT 960

GCCTGTCCTG GGAGAGACCG GCGCACAGAG GAAGAGAATC TCCGCAAGAA AGGGGAGCCT 1020

CACCACGAGC TGCCCCCAGG GAGCACTAAG CGAGCACTGC CCAACAACAC CAGCTCCTCT 1080

CCCCAGCCAA AGAAGAAACC ACTGGATGGA GAATATTTCA CCCTTCAGAT CCGTGGGCGT 1140

GAGCGCTTCG AGATGTTCCG AGAGCTGAAT GAGGCCTTGG AACTCAAGGA TGCCCAGGCT 1200

GGGAAGGAGC CAGGGGGGAG CAGGGCTCAC TCCAGCCACC TGAAGTCCAA AAAGGGTCAG 1260

TCTACCTCCC GCCATAAAAA ACTCATGTTC AAGACAGAAG GGCCTGACTC AGACTGA 1317

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln
1 5 10 15

Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu
20 25 30

Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp
35 40 45

Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro
50 55 60

Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Ala Pro Ala Ala Pro
65 70 75 80

Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser
85 90 95

Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly
100 105 110

Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro
115 120 125

Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln
130 135 140

Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met
145 150 155 160

Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys
165 170 175

Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln
180 185 190

His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp
195 200 205

Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu
210 215 220

Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser
225 230 235 240

Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr
245 250 255

Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val
260 265 270

Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn
275 280 285

Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr
290 295 300

Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys
305 310 315 320

Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu
325 330 335

Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp
340 345 350

Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His
355 360 365

Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met
370 375 380

Phe Lys Thr Glu Gly Pro Asp Ser Asp
385 390

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mus spretus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Ala Met Glu Glu Ser Gln Ser Asp Ile Ser Leu Glu Leu Pro
1 5 10 15

Leu Ser Gln Glu Thr Phe Ser Gly Leu Trp Lys Leu Leu Pro Pro Glu
20 25 30

Asp Ile Leu Pro Ser Pro His Cys Met Asp Asp Leu Leu Leu Pro Gln
35 40 45

Asp Val Glu Glu Phe Phe Glu Gly Pro Ser Glu Ala Leu Arg Val Ser
50 55 60

Gly Ala Pro Ala Ala Gln Asp Pro Val Thr Glu Thr Pro Gly Pro Val
65 70 75 80

Ala Pro Ala Pro Ala Thr Pro Trp Pro Leu Ser Ser Phe Val Pro Ser
85 90 95

Gln Lys Thr Tyr Gln Gly Asn Tyr Gly Phe His Leu Gly Phe Leu Gln
100 105 110

Ser Gly Thr Ala Lys Ser Val Met Cys Thr Tyr Ser Pro Pro Leu Asn
115 120 125

Lys Leu Phe Cys Gln Leu Val Lys Thr Cys Pro Val Gln Leu Trp Val
130 135 140

Ser Ala Thr Pro Pro Ala Gly Ser Arg Val Arg Ala Met Ala Ile Tyr
145 150 155 160

Lys Lys Ser Gln His Met Thr Glu Val Val Arg Arg Cys Pro His His
165 170 175

Glu Arg Cys Ser Asp Gly Asp Gly Leu Ala Pro Pro Gln His Leu Ile
180 185 190

Arg Val Glu Gly Asn Leu Tyr Pro Glu Tyr Leu Glu Asp Arg Gln Thr
195 200 205

Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu Ala Gly Ser
210 215 220

```
Glu Tyr Thr Thr Ile His Tyr Lys Tyr Met Cys Asn Ser Ser Cys Met
225                 230                 235                 240

Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp
                245                 250                 255

Ser Ser Gly Asn Leu Leu Gly Arg Asp Ser Phe Glu Val Arg Val Cys
            260                 265                 270

Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn Phe Arg Lys
        275                 280                 285

Lys Glu Val Leu Cys Pro Glu Leu Pro Pro Gly Ser Ala Lys Arg Ala
    290                 295                 300

Leu Pro Thr Cys Thr Ser Ala Ser Pro Pro Gln Lys Lys Lys Pro Leu
305                 310                 315                 320

Asp Gly Glu Tyr Phe Thr Leu Lys Ile Arg Gly Arg Lys Arg Phe Glu
                325                 330                 335

Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala His Ala
            340                 345                 350

Thr Glu Glu Ser Gly Asp Ser Arg Ala His Ser Ser Tyr Leu Lys Thr
        355                 360                 365

Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Thr Met Val Lys Lys
    370                 375                 380

Val Gly Pro Asp Ser Asp
385                 390
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Arg Ala His Ser Ser His Leu Lys Ser Lys Lys
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
His Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser
1 5 10 15

Arg His Lys Lys
20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser His Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys
1 5 10 15

Leu Met Phe Lys
20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser
1 5 10 15

Arg His Lys Lys Leu Met Phe Lys
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly Gln Ser Thr
1 5 10 15

Ser Arg His Lys Lys Leu Met Phe Lys
20 25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly Gln
1 5 10 15

Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys
20 25

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Lys Lys Ser Lys Leu His Ser Ser His Ala Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Ala His Ser Ser His Leu Lys
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Leu Lys Ser Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

His Leu Lys Ser Lys
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Lys Ser Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys Ser Lys Lys Gly Gln
1 5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Lys Ser Lys Lys Gly
1 5

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg Ala His Ser His Leu Lys
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

His Lys Ser Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Cys Gly Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly
1 5 10 15

Gln Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys
20 25

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Cys Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly Gln
1 5 10 15

Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys
20 25

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Gly Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly
1 5 10 15

Gln Ser Thr Ser Arg His Lys Lys Leu Met Lys
20 25

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Cys Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly Gln
1 5 10 15

Ser Thr Ser Arg His Lys Lys Leu Met Lys
20 25

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAATTCAACC AGCAGCCTCC CGCGACCATG GAGGAGCCGC AGTCAGATCC TAGCGTCGAG 60

CCCCCTCTGA GTCAGGAAAC ATTTTCAGAC CTATGGAAAC TACTTCCTGA AAACAACGTT 120

CTGTCCCCCT TGCCGTCCCA AGCAATGGAT GATTTGATGC TGTCCCCGGA CGATATTGAA 180

CAATGGTTCA CTGAAGACCC AGGTCCAGAT GAAGCTCCCA GAATGCCAGA GGCTGCTCCC 240

CCCGTGGCCC CTGCACCAGC AGCTCCTACA CCGGCCGCCC CTGCACCAGC CCCCTCCTGG 300

CCCCTGTCAT CTTCTGTCCC TTCCCAGAAA ACCTACCAGG GCAGCTACGG TTTCCGTCTG 360

GGCTTCTTGC ATTCTGGGAC AGCCAAGTCT GTGACTTGCA CGTACTCCCC TGCCCTCAAC 420

AAGATGTTTT GCCAACTGGC GAAGACCTGC CCTGTGCAGC TGTGGGTTGA TTCCACACCC 480

CCGCCCGGCA CCCGCGTCCG CGCCATGGCC ATCTACAAGC AGTCACAGCA CATGACGGAG 540

GTTGTGAGGC GCTGCCCCCA CCATGAGCGC TGCTCAGATA GCGATGGTCT GGCCCCTCCT 600

CAGCATCTTA TCCGAGTGGA AGGAAATTTG CGTGTGGAGT ATTTGGATGA CAGAAACACT 660

TTTCGACATA GTGTGGTGGT ACCCTATGAG CCGCCTGAGG TTGGCTCTGA CTGTACCACC 720

ATCCACTACA ACTACATGTG TAACAGTTCC TGCATGGGCG GCATGAACCG GAGGCCCATC 780

CTCACCATCA TCACACTGGA AGACTCCAGT GGTAATCTAC TGGGACGGAA CAGCTTTGAG 840

GTGCGTGTTT GTGCCTGTCC TGGGAGAGAC CGGCGCACAG AGGAAGAGAA TCTCCGCAAG 900

AAAGGGGAGC CTCACCACGA GCTCCCCCCA GGGAGCACTA AGCGAGCACT GCCCAACAAC 960

ACCAGCTCCT CTCCCCAGCC AAAGAAGAAA CCACTGGATG GAGAATATTT CACCCTTCAG 1020

ATCCGCGGGC GTGAGCGCTT CGAAATGTTC CGAGAGCTGA ATGAGGCCTT GGAACTCAAG 1080

GATGCCCAGG CTGGGAAGGA GCCAGGGGGG AGCAGGGCTC ACTCCAGCCA CCTGAAGTCC 1140

AAAAAGGGTC AGTCTACCTC CCGCCATAAA AAACTCATGT TCAAGACAGA AGGGCCTGAC 1200

TCAGACTGAG TCGAC 1215

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAGAGCCCCA GTTACCATAA CTACTCT 27

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATCACGTGAT ATCACGTGAT ATCACGTGAT 30

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCCGAACATG TCCCAACATG TTGGGG 26

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TCGAGCATGT TCGAGCATGT TCGAGCATGT 30

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCGGGCATGT CCGGGCATGT CCGGGCATGT 30

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Lys Ser Lys Lys Gln
1 5

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Arg Ala His Ser Ser His Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

His Leu Lys Ser Arg His
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGGCATGTCA TGGCATGTCA 20